

REMARKS

Applicant has submitted a substitute paper copy of the Sequence Listing and substitute computer readable form (CRF) copy, to address the examiner's objections. The undersigned hereby states that the substitute computer readable form (CRF) copy of the Sequence Listing and the paper copy of the Sequence Listing for the above-captioned application, in accordance with 37 C.F.R. § 1.821 through 1.825, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned application is respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made".

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to Deposit Account No. 03-1952 referencing docket no. 511582000820. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: June 12, 2002

By: Kate H. Murashige
Kate H. Murashige
Registration No. (29,959)

Morrison & Foerster LLP
3811 Valley Centre Drive
Suite 500
San Diego, California 92130-2332
Telephone: (858) 720-5112
Facsimile: (858) 720-5125

VERSION WITH MARKINGS TO SHOW CHANGES MADE

The paragraph starting at line 18, page 29, has been amended as follows:

Additional illustrative embodiments of the invention disclosed herein include 20P1F12/TMPRSS2 polypeptides containing the amino acid residues of one or more of the biological motifs contained within the 20P1F12/TMPRSS2 polypeptide sequence as shown in FIG. 1 (and the polynucleotides encoding these polypeptides). In one embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 N-glycosylation sites such as NTSA at residues 213-216 and/or NSSR at residues 249-252. In another embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 Protein Kinase C phosphorylation sites such as TSK at residues 78-80, TSK at residues 447-449, TKK at residues 81-83, SQR at residues 163-165, SSK at residues 232-234, SLR at residues 238-240, SSR at residues 250-252, and/or TQR at residues 407-409. In another embodiment, typical polypeptides of the invention can contain one or more of the 20P1F12/TMPRSS2 casein kinase II phosphorylation sites such as TVYE at residues 35-38, SGIE at residues 116-119 and/or TFND at residues 356-359. In another embodiment, typical polypeptides of the invention can contain one or more of the N-myristoylation sites such as GSPPAI (SEQ ID NO: 30) at residues 6-11, GTVCTS (SEQ ID NO:31) at residues 74-79, GAALAA (SEQ ID NO: 32) at residues 97-102, GSKCSN (SEQ ID NO: 33) at residues 110-115, GVNLSN (SEQ ID NO: 34) at residues 245-250, GGESAL (SEQ ID NO: 35) at residues 258-263, GNVDSN (SEQ ID NO: 36) at residues 432-437, GSGCAK (SEQ ID NO: 37) at residues 462-467, GCAKAY (SEQ ID NO: 38) at residues 464-469 and/or GVYGN (SEQ ID NO: 39) at residues 472-477. In another embodiment, typical polypeptides of the invention can contain the ATP/GTP-binding site motif A (P-loop), ATECKGKT (SEQ ID NO: 40) at residues 386-393. In another embodiment, typical polypeptides of the invention can contain the LDL-

receptor class A (LDLRA) domain signature CINPSNWCDGVSHCPGGEDENRC (SEQ ID NO: 41) at residues 126-148. In another embodiment, typical polypeptides of the invention can contain the Serine proteases, trypsin family, histidine active site VTAAHC (SEQ ID NO: 42) at residues 292-297. In another embodiment, typical polypeptides of the invention can contain the Serine proteases, trypsin family, serine active site DSCQGDSGGPLV (SEQ ID NO: 43) at residues 435-446. Related embodiments of these inventions include polypeptides containing combinations of the different motifs discussed above with preferable embodiments being those which contain no insertions, deletions or substitutions either within the motifs or the intervening sequences of these polypeptides.